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OM protein - protein search, using sw model

Run on: November 4, 2002, 12:20:59 : Search time 21 seconds

Scoring table: 2512.050 Million cell updates/sec

(without alignments)

Title: US-09-972-26B-6

Perfect score: 549

Sequence: 1 MARTLRLRSPPLCPGGKQLS.....EDDLVSHVDGSQLSRREWVY 549

Scoring table: OLIGO

Searched: Gap0 60.0 , Gappext 60.0

Result size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Result No.	Score	Query Length	DB ID	Description
1	322	58.7	T09732	hypothetical protein
2	8	1.5	100	hypothetical prote
3	8	1.5	106	hypothetical prote
4	8	1.5	132	proline/leucine-rich
5	8	1.5	266	Ig light chain V region
6	8	1.5	293	conserved hypothetical protein
7	8	1.5	341	hypothetical protein
8	8	1.5	342	probable membrane protein
9	8	1.5	342	T45456
10	8	1.5	452	JC7110
11	8	1.5	469	brain specific membrane protein
12	8	1.5	470	KCHOT
13	8	1.5	470	AD1430
14	8	1.5	503	transmembrane efflux protein
15	8	1.5	503	probable sodium transporter
16	8	1.5	513	probable membrane protein
17	8	1.5	513	WDR991
18	8	1.5	594	hypothetical protein
19	8	1.5	606	interstitial collagen
20	8	1.5	607	transmembrane efflux protein
21	8	1.5	694	dehydrogenase
22	8	1.5	743	probable transketolase
23	8	1.5	761	probable membrane protein
24	8	1.5	787	probable tyrosine receptor
25	8	1.5	920	tyrosine receptor
26	8	1.5	1309	dehydrogenase
27	8	1.5	1622	peptidyl-dipeptidase
28	7	1.3	51	DNA (cytosine-5)-
29	7	1.3	87	acetylcholinesterase
7	7	1.3	87	30S ribosomal protein

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Db 1 SGKYICKAVTTEPLGNAQSTVTVLVEPVSLKGPPDSLIGNGNEVAACIATGKPV A 60
 Qy 203 HIDRPGDGLGEMSTTSFPPNETATISQYKLFTRFARCRERITCIVKHALEDIYSFI 262
 Db 61 HIDRPGDGLGEMSTTSFPPNETATISQYKLFTRFARCRERITCIVKHALEDIYSFI 120
 Qy 263 LDIQYAPEVSVQIGWFGVGRKGUNLKNQADANPPFKSWRLGDQMPDGLASNTL 322
 Db 121 LDIQYAPEVSVQIGWFGVGRKGUNLKNQADANPPFKSWRLGDQMPDGLASNTL 180
 Qy 323 HFVHLTENSGWVICKVTLQGQSDKRYVYISDPTTILQPTQWHPSSTADIELAT 382
 Db 181 HFVHLTENSGWVICKVTLQGQSDKRYVYISDPTTILQPTQWHPSSTADIELAT 240
 Qy 383 EPKKLUPPLFPLSTLAKDTITIISWGGALFIVLVSAGIFYRRRTFRGDFAKN 442
 Db 241 EPKKLUPPLFPLSTLAKDTITIISWGGALFIVLVSAGIFYRRRTFRGDFAKN 442
 Qy 443 YIPPSDMQESQIDVLOQDELD 464
 Db 301 YIPPSDMQESQIDVLOQDELD 322

RESULT 2
 H71133 hypothetical protein PH0836 - Pyrococcus horikoshii
 C;Species: Pyrococcus horikoshii
 C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
 C;Accession: H71133
 R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seir M.; Ohfuki, Y.; Runashiki, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A;Reference number: A71000; MUID:9844137
 A;Accession: H71133
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-100 <S&W>
 A;Cross-references: GB:AP00003; NID:93236130; PIDN:BAK29930.1; PID:93257247
 A;Experimental source: strain OJ3
 C;Note: this accession replaces an interim accession for a sequence replaced by GenBank
 A;Gene: PH0836
 C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0836
 Query Match 1.5%; Score 8; DB 2; length 132;
 Best Local Similarity 100.0%; Pred. No. 8.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 41 LLLFPILL 48
 Db 6 LLLFPILL 13

RESULT 5
 G83178 conserved hypothetical protein PA3747 [imported] - pseudomonas aeruginosa (strain PA
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: G83178
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.;
 ; Mori, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic p
 A;Reference number: A82950; MUID:20337337
 A;Accession: G83178
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-266 <S&D>
 A;Cross-references: GB:AE04793; GB:AE04091; NID:99949904; PIDN:AAG07134.1; GSPDB:G
 A;Experimental source: strain PA01
 C;Genetics:
 T06479 proline-leucine-rich protein precursor - garden pea
 C;Species: Pisum sativum (garden pea)
 C;Date: 22-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Nov-1999
 C;Accession: T06479
 R;Rodríguez-Concepción, M.; Pérez-García, A.; Beltrán, J.
 submitted to the EMBL Data Library, November 1995
 A;Description: Isolation of cDNAs which accumulate during pea (Pisum sativum L.) early f
 A;Reference number: 215708
 A;Accession: T06479
 A;Status: preliminary; translated from GB/EMBL/DDB3
 A;Molecule type: mRNA
 A;Residues: 1-106 <S&D>
 A;Cross-references: EMBL:267873; NID:91213129; PIDN:CAA91780.1; PID:e208986
 C;Domain: signal sequence #status predicted <SIG>
 C;Product: proline-leucine-rich protein #status predicted <MAT>
 S47094 S47094
 hypothetical protein - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S47094

Query Match 1.5%; Score 8; DB 2; length 106;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 36 PPLLUU 43
 Db 79 PPLLUU 86

RESULT 4
 A55410 Ig light chain V region (variant CA2) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
 C;Accession: A55410
 R;Tachibana, H.; Kido, I.; Murakami, H.
 J; Biol. Chem. 269, 29051-29065, 1994
 A;Title: Heterogeneous expression of human antibody lambda chains by concanavalin A
 A;Reference number: A55410; MUID:95050725
 A;Accession: A55410
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-132 <S&C>
 A;Cross-references: GB:ST4107
 C;Superfamily: immunoglobulin
 F:35-114/Domain: immunoglobulin homology <IMM>
 C;Keywords: immunoglobulin
 F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 1.5%; Score 8; DB 2; length 132;
 Best Local Similarity 100.0%; Pred. No. 8.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 41 LLLFPILL 48
 Db 6 LLLFPILL 13

RESULT 6
 S47094 S47094
 hypothetical protein - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S47094

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Om protein - protein search, using sw model

Run on: November 4, 2002, 12:02:17 ; Search time 6.76126 Seconds (without alignments)

Sequence: US-09-972-268-6_COPY_74_152

Scoring table: BL2SUM62

Gappen 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Maximum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRREMBL_19;*

1: sp_archaeal;*

2: sp_bacteria;*

3: sp_fungi;*

4: sp_human;*

5: sp_invertebrate;*

6: sp_mammal;*

7: sp_mhc;*

8: sp_organelle;*

9: sp_phage;*

10: sp_plant;*

11: sp_prok;*

12: sp_virus;*

13: sp_vertebrate;*

14: sp_unclassified;*

15: sp_virus;*

16: sp_bacteria;*

17: sp_archeap;*

pred - No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description	
1	416	100.0	549	4_09N053	Q9NQ33 homo sapien	
2	410	99.6	438	1_09J1B7	Q9J1B7 mus musculu	
3	410	98.6	510	1_09J1B8	Q9J1B8 mus musculu	
4	410	98.6	549	1_09D046	Q9D046 mus musculu	
5	410	98.6	549	1_09J1B9	Q9J1B9 mus musculu	
6	32.9	295	549	1_09G125	Q9G125 bos taurus	
7	31.7	295	11	Q9E953	Q9E953 mesocricetus	
8	131.5	31.6	6	Q9G174	Q9G174 cecropi <th>thec</th>	thec
9	114.5	27.5	261	1_09D049	Q9D049 mus musculu	
10	114.5	27.5	408	1_09W01	Q9W01 mus musculu	
11	109.5	26.3	336	4_015762	Q5762 homo sapien	
12	109.5	26.3	336	6_046551	Q6551 hylobates s	
13	108.5	26.1	336	6_018905	Q18905 macaca mula	
14	103	24.8	269	4_09H313	Q9H313 homo sapien	
15	103	24.8	271	12_049048	Q49048 kaposi's sa	
16	103	24.8	348	12_P88963	P88963 kaposi's sa	

ALIGNMENTS

RESULT 1

Q9NQ33	PRELIMINARY;	PRT;	549 AA.
Q9NQ33;	AC;		
DT 01-OCT-2000	(TREMBREL_15, Created)		
DT 01-OCT-2000	(TREMBREL_15, Last sequence update)		
DT 01-DEC-2001	(TREMBREL_19, Last annotation update)		
DE NECTIN_3.			
DS Homo sapiens (Human)			
OC Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarhini; Homidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
SEQUENCE FROM N_A.			
RA Raymond N., Borg J.-P., Lecocq B., Adelaide J., Campadelli-Fiume G.,			
RA Dubreuil P., Lopez M.; A novel member of the PVR/PRR/hectin family that			
RT Human hectin 3 (PRR).			
RT interacts with afadin.;			
RT genes 0-0 (2000).			
DR EMBL: AAF28284; AAF97597.1; -.			
DR InterPro: IPR00359; Ig.			
DR InterPro: IPR00360; Ig-like.			
DR InterPro: IPR031006; Ig_MHC.			
DR Pfam: PF0007; Ig_1.			
DR SMART: SM00409; Ig_1.			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA; 61002 MW;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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DR SEQUENCE: 549 AA;			
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DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
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DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
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DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
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DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
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DR SMART; SM00110; Ig_Like_1.			
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DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
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DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
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DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1.			
DR SEQUENCE: 549 AA;			
DR SO 6D1104CCB4A0D731 CRC64;			
DR Query Match 100.0%; Score 416. DB 4; Length 549;			
DR Best Local Similarity 100.0%; Pred. No. 1e-39;			
DR Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR SMART; SM00110; Ig_Like_1			

RESULT 2	PRELIMINARY;	PRT;	438 AA.	DR InterPro; IPR003006; Ig_MHC.
09JLB7	PRELIMINARY;	PRT;	438 AA.	DR Pfam; PF00047; Ig; 2.
09JLB7;	PRT;	438 AA.	DR SMART; SM00409; Ig; 1.	
AC 09JLB7;	PRT;	438 AA.	DR SEQUENCE; SM00410; Ig_like; 1.	
DT 01-OCT-2000 (Tremblel, 15, Created)			Query Match 98.6%; Score 410; DB 11; Length 510;	
DT 01-OCT-2000 (Tremblel, 15, Last sequence update)			Best Local Similarity 97.5%; Pred. No. 4 Ig-39;	
DT 01-DEC-2001 (Tremblel, 19, Last annotation update)			Mismatches 0; Indels 0; Gaps 0;	
DE CELL ADHESION MOLECULE NECTIN-3 GAMMA.			DR Matches 77; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
GN PVR3.			DR	
OS Mus musculus (Mouse).			QY 1 VSLKCLIEVNETITQISWEKIHKGKSSQTAVHHRPOYFSVQGEYQGRVLFKNYSNDATI 60	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			Db 74 VSLKCLIEVNETITQISWEKIHKGKSSQTAVHHRPOYFSVQGDYQGRVLFKNYSNDATI 133	
OC NCBI_TaxID=10090;			QY 61 THNIGFSGSKYICKAVT 79	
RN [1]			Db 134 THNIGFSGSKYICKAVT 152	
RR SEQUENCE FROM N_A.			DR	
RX MEDLINE=2029400; PubMed=10744716;			Q90006	
RA Satoh-Horigawa K., Nakashishi H., Takahashi K., Miyahara M.,			PRELIMINARY;	
RT *Nectin-3: a new member of immunoglobulin-like cell adhesion molecules that shows homophilic and heterophilic cell-cell adhesion activities.;			PRT;	
RL J. Biol. Chem. 275:10291-10299(2000).			438 AA.	
DR EMBL; AF053675; MAF3675.1; -			DR	
DR MGD; MGI:1930171; P013.			DR	
DR InterPro; IPR003599; Ig_like.			DR	
DR InterPro; IPR003600; Ig_MHC.			DR	
DR InterPro; IPR003006; Ig_MHC.			DR	
DR Pfam; PF00047; Ig; 2.			DR	
DR SMART; SM00409; Ig; 1.			DR	
SO SEQUENCE 438 AA; 47210 MN; 2A0A4416E5B02FEF CRC64;			DR	
Best Local Similarity 97.5%; Score 410; DB 11; Length 438;			DR	
Matches 77; Conservative 2; Mismatches 0; Indels 0; Gaps 0;			DR	
QY 1 VSLKCLIEVNETITQISWEKIHKGKSSQTAVHHRPOYFSVQGEYQGRVLFKNYSNDATI 60			DR	
Db 74 VSLKCLIEVNETITQISWEKIHKGKSSQTAVHHRPOYFSVQGDYQGRVLFKNYSNDATI 133			DR	
QY 61 THNIGFSGSKYICKAVT 79			DR	
Db 134 THNIGFSGSKYICKAVT 152			DR	
RESULT 3			DR	
JLB8 PRELIMINARY;	PRT;	510 AA.	DR	
RC 09JLB8 PRELIMINARY;	PRT;	510 AA.	DR	
DT 01-OCT-2000 (Tremblel, 15, Created)			DR	
DT 01-OCT-2000 (Tremblel, 15, Last sequence update)			DR	
DT 01-DEC-2001 (Tremblel, 19, Last annotation update)			DR	
DE CELL ADHESION MOLECULE NECTIN-3 BFR.			DR	
GN PVR3.			DR	
OS Mus musculus (Mouse).			DR	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			DR	
OC NCBI_TaxID=10090;			DR	
RN [1]			DR	
RR SEQUENCE FROM N_A.			DR	
RX MEDLINE=2029400; PubMed=11217851;			DR	
RA Kawai J., Shinagawa A., Sibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hira S., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arizawa T., Iwasa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H., Ashburner M., Battaglia S., Casavant T., Fischmann W., Gaasterland T., Giasi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nakauchi T., Pesoite G., Quackenbush J., Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G., Blak J., Boffelli D., Bojunga N., Carnici P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garkiobi M., Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamila M., Lee N.H., Lyons P., Marchionni J., Mazzarelli J., Mombretti P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Sessa C., Shitara Y., Storch K.-F., Suzuki H., Tayaoka K., Wang K.H., Weltz C., Whitaker C., Wilmung L., Wynnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;			DR	
RT Functional annotation of a full-length mouse cDNA collection.;			DR	
RL Nature 409:688-690(2000).			DR	
DR EMBL; AK011949; BAB27033.1;			DR	
DR MGD; MGI:19102261030119RIK.			DR	
DR InterPro; IPR003599; Ig.			DR	
DR InterPro; IPR003600; Ig_like.			DR	
DR InterPro; IPR003006; Ig_MHC.			DR	
DR Pfam; PF00047; Ig; 2.			DR	
DR SMART; SM00409; Ig; 1.			DR	
DR SEQUENCE 549 AA; 60703 MN; 32775C8C7319832 CRC64;			DR	
Best Local Similarity 97.5%; Score 410; DB 11; Length 549;			DR	
Matches 77; Conservative 2; Mismatches 0; Indels 0; Gaps 0;			DR	
QY 1 VSLKCLIEVNETITQISWEKIHKGKSSQTAVHHRPOYFSVQGEYQGRVLFKNYSNDATI 60			DR	
Db 74 VSLKCLIEVNETITQISWEKIHKGKSSQTAVHHRPOYFSVQGDYQGRVLFKNYSNDATI 133			DR	

